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## FIG. 1A

GAATTCCGCGTCGAATCATTGCTGTTGGTATCGATTCAAGAACGAAACTTGTGATCGA  
 1 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60  
 TAACAAGTCATTCAAACACGGCGAAGATGTCTATCGTATAACAGAATATTGGAGAAAT  
 61 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120  
 GCTCGCAAAACTCGAAATTGTCACCGATAAAATGATTAACCTTGAGGGGCTAATGTAAGT  
 121 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180  
 TATCTGATGTTCTACAATTAAAAAAATTGTTTTTCCAAATTAAATTTCGAAGATT  
 181 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240  
 AACGAAAACGATTAACAAATCAATAACGCAATAAGAGGGCTGGCTTCTTTAAAT  
 241 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 300  
 TTAAATTATAATTTCGATTGTTGTATGAAGCTACAAATGTACTGTTTGATTTG  
 301 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360  
 AATATTGTATTACAGGGTTGGGATTCTCGCAAATATCAGCGACAGTGGAAAGATTTAGAA  
 361 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420  
 GAAGGACGTGTGACAATCACTAAGTCAAAGAGGGAAAGGATAAAGGATTGTGATATTCA  
 421 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480  
 CTGTTTACTCATCGCTTTAAATAAGAACTATATGCCGATTGCCATATATTG  
 481 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540  
 TTTATTAGGCCTCTCACATTCTGTACAATGTTCTACAAATAACTGCATTTATCT  
 541 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600  
 GAAAATTGAAATTATTTTGCTACTTTTACTCGTTGCATCGAGATCAGCATATCTT  
 601 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660  
 CCGGTCTATTATATTCAACGATTTATAAATTAGTACTCCTTCATGTTAATTTCATT  
 661 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720  
 TTATCTGTAAGCTTACTGTATTTTAAATCTTCTGCTTCTATCTGATTACAA  
 721 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 780  
 TGTTCTTACTCATTTCAAGGTATTTTATGCCCTCACAAATTATGCACATTCGGGCTT  
 781 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840  
 GGAGATTATCCTCTATATTACATGCCGTTTTTAAAGGATATAATGTTAACAAATA  
 841 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900  
 ATTTTTATCAATGCTATTGTATATTCTCCAGCTAACCGTTGGCGAAACATCACCTA  
 901 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 960  
 GCATTTAAAATTCACAAACTTGCTCCTATAATCAAGAAGATTTCAGATGCTCT  
 961 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020  
 M L C  
 1↓  
 GCGAAATCGAATGCCCGCTTGAGCACGGCACACACGAGGCTCATCCACGACTTGAAC  
 1021 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080  
 E I E C R A L S T A H T R L I H D F E P  
 10 20  
 T n1162  
 ↑  
 CACGTGACGCATTGACTTATTTAGAAGGAAAAACATTTCACAGAAGATCATTCTGAAC  
 1081 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140  
 R D A L T Y L E G K N I F T E D H S E L  
 30 40  
 TTATCAGTAAAATGTCAACTGCCCTCGAGAGGATGCCAATTTCTCGAATCTATCGAC  
 1141 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200  
 I S K M S T R L E R I A N F L R I Y R R  
 50 60  
 GTCAAGCTTCTGAACCTGGACCACTCATGACTTTCAACTACAACAATCAAAGTCACC  
 1201 +-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260  
 Q A S E L G P L I D F F N Y N N Q S H L  
 70 80

Title: CLONING, SEQUENCING AND CHARACTERIZATION  
 OF TWO CELL DEATH GENES AND USES THEREFOR  
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 Serial No.: 08/984,178  
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**FIG. 1B**

```

TTGCTGATTCCTCGAAGACTACATCGATTCGATAATGAGCCAGATCTACTTCGTC 1320
1261 -----+-----+-----+-----+-----+
          A D F L E D Y I D F A I N E P D L L R P
          90                                100
CAGTAGTGATTGCTCCACAATTTCCCACAAATGCTCGATAGGAAACTATTGCTTGGGA 1380
1321 -----+-----+-----+-----+-----+
          V V I A P Q F S R Q M L D R K L L L G N
          110                                120
                                         T n2274
                                         ↑
ATGTTCAAAACAAATGACATGCTATATCGAGAGTATCACGTGGATCGAGTGATCAAAA 1440
1381 -----+-----+-----+-----+-----+
          V P K Q M T C Y I R E Y H V D R V I K K
          130                                140
                                         Intron 1
AGCTCGACGAGATGTGTGATTAGGTGAGAAAATCTGGAAGCTCTCGTGTATTATAATC 1500
1441 -----+-----+-----+-----+-----+
          L D E M C D L D
          150
TTGCTTAAACTTCAGACTCCCTTTCTGTTCTACACGGCCGAGCTGGATCCGGAAAAT 1560
1501 -----+-----+-----+-----+-----+
          S F F L F L H G R A G S G K S
          160
                                         Intron 2
CAGTAATTGCATCACAGCTTTGAAATCTGACCAACTTATTGGAATGTGAGTGGTAT 1620
1561 -----+-----+-----+-----+-----+
          V I A S Q A L S K S D Q L I G I
          170                                180
TATCTGAATCTACGGATCTTCATTCTATTACAGAAATTATGATTCAATCGTTGGCTCAA 1680
1621 -----+-----+-----+-----+-----+
          N Y D S I V W L K
          190
AGATAGTGGAACAGCTCCAAAATCTACATTGATTATTCACGGATATTGCTGATGCT 1740
1681 -----+-----+-----+-----+-----+
          D S G T A P K S T F D L F T D I L L M L
          200                                210
                                         A n1920/n2247
                                         ↑ Intron 3
AAAGTGAGTGAATAGAGTGCATGTAACATTGAGCATGATTTGAAATTATGAAAATTG 1800
1741 -----+-----+-----+-----+-----+
          K
CCTGGTTAGCTTTAATTGATATTGCTGACGCTTGCATGTTGTGTGAAAGACG 1860
1801 -----+-----+-----+-----+-----+
          AGCCCGTGTGTGAGCGACACGGATGACTCGATCACCAGCTTCATTAACCGTGT
          1861 -----+-----+-----+-----+-----+
                                         A n2273
                                         ↑
TCTTTCAAGAAGCGAAGACGATCTCTCAATTCCATCGTGGAGCATGTCACGTCAGT 1920
1921 -----+-----+-----+-----+-----+
          S E D D L L N F P S V E H V T S V
          220

```



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## FIG. 1C

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Intron 4

1981	<pre> TGTACTCAAAGGATGGTAAGTTGCCGATTCTGGTACAATATCTAAATTATTGGT V L K R M </pre>	2040
2041	<pre> 230 TTTTAGATCTGCAACGCACTCATTGATCGTCAAATACCTTATTGTATTGATGACGTA I C N A L I D R P N T L F V F D D V </pre>	2100
	240                    250 A n1948            T n1947 ↑                    ↑	
2101	<pre> GTTCAAGAAGAAACAATTCTGGCTCAGGAGCTACGTCTCGATGTCTGTAACTACT V Q E E T I R W A Q E L R L R C L V T T </pre>	2160
	260                    270	
2161	<pre> CGTGACGTGGAAATATCAAATGCTGCTCTCAAACATGCGAATTGAAAGTGACATCA R D V E I S N A A S Q T C E F I E V T S </pre>	2220
	280                    290	
2221	<pre> TTGGAAATCGATGAATGTTATGATTCTAGAACGCTTATGGAATGCCATGCCTGTTGGA L E I D E C Y D F L E A Y G M P M P V G </pre>	2280
	300                    310 Tc4 n1416 ↓	
2281	<pre> GAAAAAGAAGATGTGCTTAATAAAACAATCGAACTAACAGTGGAAATCCAGCAACG E K E E D V L N K T I E L S S G N P A T </pre>	2340
	320                    330	
2341	<p style="text-align: center;">Intron 5</p> <pre> CTTATGATGTTTCAGTCTTGTGAACCGAAAACATTGAAAAGTGAGTGGACATACC L M M F F K S C E P K T F E K </pre>	2400
	330	
2401	<pre> AATTGAGACTTTAAAATAATTCTACAATAAAAGTTAATCAAAAGTTCATAGC TGATTGTCTTAAATTACGAATTGAGGATCAAAATCAAGAATTAGGATCCTGGCACGA </pre>	2460
2461	<pre> GAGAAAATGTGTAGCTACCGTACCCGAGAGATTCTTGATATTGCCATCGATTAAAT </pre>	2520
2520	<pre> TTTTAAGAAAATTATCGTTTACATAATTGAACAAGAGATAACCGGTCTGACCCGACG </pre>	2580
2581	<pre> GAAATTTTAAATGAAAGCGAGTATGAGCCTGTTCATTATTTGATTTCTCTTG </pre>	2640
2641	<pre> TTGTTCTTTATTAAAGCCTTTATTGAAACAAGTCTAAAATATTAAAAACTGA </pre>	2700
2701	<pre> ATAAAATATTAAAAAAATCAAGTAAAATAGAAAAACAGCAAGGCTGGAGACTACTGTA </pre>	2760
2760	<pre> CTTCTAAATCCGCATACTCTTTATTAAATCATTCCGAATGTCGAAACGAAATAA </pre>	2820
2821	<pre> TACATTTAGTCCAAATCGCTAGGTATATTCTAAAATTATCAAACATTTGCATTCA </pre>	2880



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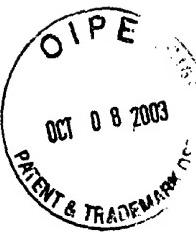
Billing Date: 12/01/08



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FIG. 1E

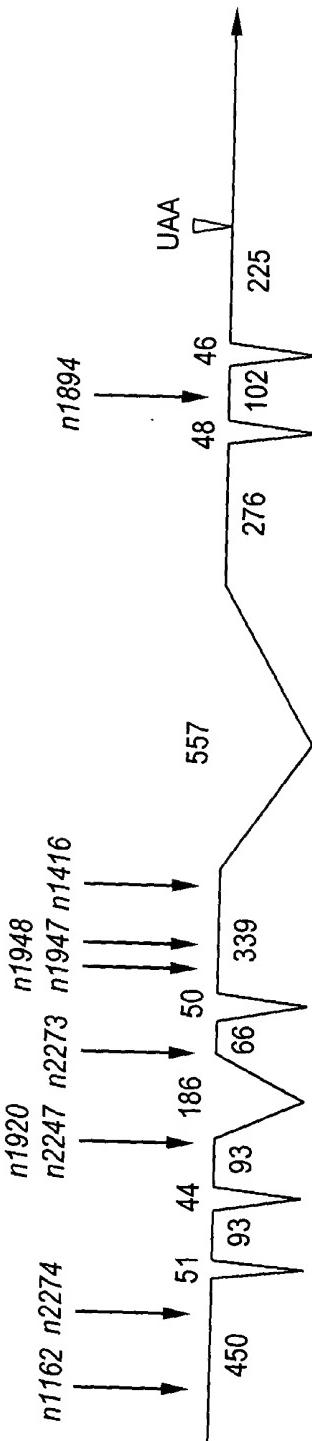
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FIG. 2





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## FIG. 3

	10	12	14		18	21
	X	Y	Z		-X	-Z
	D	N	S		T	E
Calcium-binding loop consensus		D	N		S	
			D		E	
					Q	
					D	
					N	
EF-hand consensus	O	*	O	G	*	*
					O	*
ced-4 sequence 1	Y	N	N	Q	S	H
	L	A	D	F	L	E
sequence 2	S	L	E	I	D	E
	C	Y	D	F	L	E
Parvalbumin (carp)	D	Q	D	K	S	G
(hake)	D	Q	D	K	D	D
(ray)	D	S	D	G	D	H
	F	I	E	E	E	E
	E	D	F	I	G	E
	D	S	K	I	G	V
	E	D	E	D	E	E
SCBP ( <i>Amphioxus I</i> )	D	I	N	K	D	D
	V	V	S	W	E	E
ICaBP (bovine)	A	K	E	G	D	P
	D	K	N	G	D	G
	S	K	E	V	S	F
	E	E	E	E	E	E
Troponin C (rabbit)	D	A	D	G	G	G
	D	E	D	G	S	G
	R	N	A	D	G	Y
	D	K	N	N	D	G
	I	S	V	V	I	E
	E	E	K	E	E	E
	E	E	E	E	E	E
Calmodulin (bovine)	D	K	D	G	N	G
	T	I	T	T	K	E
Trypsinogen	L	G	E	D	N	I
	N	V	V	V	E	E
Fibrinogen	D	N	D	N	D	K
	E	G	E	N	G	F
Villin	G	V	D	P	S	R
	H	L	S	N	H	L
GBP	D	L	N	K	D	G
	Q	I	Q	I	Q	I
	I	E	I	E	I	E



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**FIG. 4A**

### **ced-3 Genomic Sequence**

**Repeat 1**

1321 TAAATCGGCTCGACATTATCGTATTAAGGAATCACAAAATTCTGAGAATGCGTACTGC  
1380  
1381 AACATATTGACGGCAAAATATCTCGTAGCGAAAACATACAGTAATTCTTTAAATGACTAC  
1440



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## FIG. 4B

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Repeat 1

```

-----> -----<
TGTAGCGCTTGTGTCGATTTACGGGCTCAATTTTGAAAATAATTTTTTTGAATTT
1441 -----+-----+-----+-----+-----+-----+-----+-----+ 1500

-----<
TGATAACCCGTAATCGTCACAACGCTACAGTAGTCATTAAAGGATTACTGTAGTTCTA
1501 -----+-----+-----+-----+-----+-----+-----+-----+ 1560

-----<
GCTACGAGATATTTGCGCGCCAAATATGACTGTAATACGCATTCTCTGAATTTGTGTT
1561 -----+-----+-----+-----+-----+-----+-----+-----+ 1620
TCCGTATAATTCACAAGATTTGGCATTCCACTTAAAGGCGCACAGGATTATTCCA
1621 -----+-----+-----+-----+-----+-----+-----+-----+ 1680
ATGGGTCTCGGCACGCAAAAGTTGATAGACTTTAAATTCTCCTTGCATTTAAATTC
1681 -----+-----+-----+-----+-----+-----+-----+-----+ 1740
AATTACTAAAATTTCGTGAATTTCTGTTAAAATTTAAAATCAGTTTCTAATATT
1741 -----+-----+-----+-----+-----+-----+-----+-----+ 1800
TTCCAGGCTGACAAACAGAAACAAAAACACAACATTTAAAAATCAGTTTCAAAT
1801 -----+-----+-----+-----+-----+-----+-----+-----+ 1860
TAAAAATAACGATTCTCATCGAAAATTGTGTTTATGTTGCGAAAATAAAAGAGAACT
1861 -----+-----+-----+-----+-----+-----+-----+-----+ 1920
GATTCAAAACAATTAAACAAAAAAACCCAAAATCGCCAGAAATCAAGATAAAAAAA
1921 -----+-----+-----+-----+-----+-----+-----+-----+ 1980
TTCAAGAGGGTCAAAATTTCCGATTTACTGACTTCACCTTTTTCGTAGTTCACTG
1981 -----+-----+-----+-----+-----+-----+-----+-----+ 2040
GCAGTTGTTGGAGTTTGACGAAAATAGGAAAAAAATCGATAAAAATTACTCAAATCG
2041 -----+-----+-----+-----+-----+-----+-----+-----+ 2100
AGCTGAATTTGAGGACAATGTTAAAAAAACACTATTTCCAATAATTCACTCAT
2101 -----+-----+-----+-----+-----+-----+-----+-----+ 2160

-----<
TTTCAGACTAAATCGAAAATCAAATCGTACTCTGACTACGGGTCAGTAGAGAGGTCAACC
2161 -----+-----+-----+-----+-----+-----+-----+-----+ 2220

-----<
ATCAGCCGAAGATGATGCGTCAAGATAGAAGGAGCTTGCTAGAGAGGAACATTATGATGT
2221 -----+-----+-----+-----+-----+-----+-----+-----+ 2280
M M R Q D R R S L L E R N I M M F
1 10
T (n1040)
|
TCTCTAGTCATCTAAAGTCGATGAAATTCTCGAAGTTCTCATCGAAAACAAGTGTGA
2281 -----+-----+-----+-----+-----+-----+-----+-----+ 2340
S S H L K V D E I L E V L I A K Q V L N
20 30
| Intron 1
ATAGTGATAATGGAGATATGATTAATGTGAGTTTAATCGAATAATAATTTAAAAAA
2341 -----+-----+-----+-----+-----+-----+-----+-----+ 2400
S D N G D M I N
40

```



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## FIG. 4C

AATTGATAATATAAAGAATATTTTGCAGTCATGTGGAACGGTCGCGAGAAGAGACGGG  
 2401 -----+-----+-----+-----+-----+-----+ 2460  
 S C G T V R E K R R E  
 50  
 A (n718)  
 |  
 AGATCGTAAAGCAGTGCAACGACGGGAGATGTGGCGTTCGACCGTTTATGATGCTC  
 2461 -----+-----+-----+-----+-----+-----+ 2520  
 I V K A V Q R R G D V A F D A F Y D A L  
 60 70  
 | Intron 2  
 TTCGCTCTACGGGACACGAAGGACTTGCTGAAGTTCTGAAACCTCTGCCAGATCGTAGG  
 2521 -----+-----+-----+-----+-----+-----+ 2580  
 R S T G H E G L A E V L E P L A R S  
 80 90  
 |  
 TTTTTAAAGTCGGCGAAAAGCAAGGGCTCACGGAAAAAGAGGCGGATCGTAATTT  
 2581 -----+-----+-----+-----+-----+-----+ 2640  
 GCAACCCACCGGCACGGTTTTCTCCGAAATCGGAAATTATGCACTTCCAAATAT  
 2641 -----+-----+-----+-----+-----+-----+ 2700  
 TTGAAGTGAATATATTTTACTGAAAGCTCGAGTGATTATTTATTAAACACTA  
 2701 -----+-----+-----+-----+-----+-----+ 2760  
 ATTTCTGGCGCAAAGGCCATTGTAGATTGCCGAAAATCTGTACACACACAC  
 2761 -----+-----+-----+-----+-----+-----+ 2820  
 |  
 ACACACATCTCCTCAAATATCCCTTTCCAGTGTGACTCGAATGCTGTCGAATCGA  
 2821 -----+-----+-----+-----+-----+-----+ 2880  
 V D S N A V E F E  
 100  
 |  
 GTGTCCAATGTCACCGCAAGCCATCGTCGGAGCCGCGATTGAGCCCCGGCTACAC  
 2881 -----+-----+-----+-----+-----+-----+ 2940  
 C P M S P A S H R R S R A L S P A G Y T  
 110 120  
 |  
 TTCACCGACCCGAGTTCACCGTACAGCGTCTTCAGTGTCAATTCACTTCTTATCA  
 2941 -----+-----+-----+-----+-----+-----+ 3000  
 S P T R V H R D S V S S V S S F T S Y Q  
 130 140  
 |  
 GGATATCTACTCAAGAGCAAGATCTCGTCTCGATCGCGTGCACCCATTCACTCGGATCG  
 3001 -----+-----+-----+-----+-----+-----+ 3060  
 D I Y S R A R S R S R A L H S S D R  
 150 160  
 | Intron 3  
 ACACAATTATTCACTCCTCCAGTCAACGCATTCCCAGCCAACCTTGATGTTGATGCG  
 3061 -----+-----+-----+-----+-----+-----+ 3120  
 H N Y S S P P V N A F P S Q P S  
 170



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## FIG. 4D

### Repeat 1

3121 AACACTAAATTCTGAGAATGCGCATTACTCAACATATTCGACGGCAAATATCTCGTAGC 3180

3181 GAAAAATACAGTAACCCTTAAATGACTATTGTAGTGTGATTACGGGCTGATTTCG 3240

3241 AAACGAATATATGCTCGAATTGTGACAACGAATTAAATTGTCATTTGTGTTTCTT 3300

### Repeat 1

3301 TTGATATTTGATCAATTAATAATTATTCGTAACAGACACCAGCGCTACAGTACT 3360

3361 CTTTTAAAGAGTTACAGTAGTTTCGTTCAAGATATTGAAAAGAATTAAACATT 3420

3421 TGAAAAAAATCATCTAACATGTGCCAAACGCTTTTCAGTTTCGAGATTTTG 3480

### Repeat 2

3481 TTTTTTCATTCAAGATATGCTTATTAACACATATAATTATCATTATGTGAATTCTTG 3540

3541 TAGAAATTTGGGCTTTCTAGTATGCTCTACTTTGAAATTGCTAACGAAAAAA 3600

3601 TCATGTGGTTGTTCATATGAATGACGAAAAATAGCAATTATATATTTCCCCTAT 3660

3661 TCATGTTGTGCAGAAAAATAGTAAAAAGCGCATGCATTTGACATTACATCGA 3720

3721 ACGACAGCTCACTCACATGCTGAAGACGAGAGACGCGGAGAAATACACACATTTCT 3780

### Repeat 2

3781 GCGTCTCTCGTCTTCAGCATGTGAAATGGATCTCGGTGATGTAAAAAAATGTCGAAATA 3840

3841 ATGTAATAATGCATGCGTTTTACACTTTCTGCACAAATGAATAGGGGAAATGT 3900

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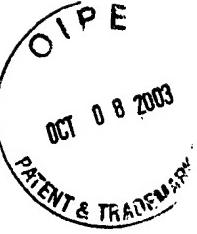


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## FIG. 4E

ATTTAAACATTTTGATTTCAACATCACATGATTAACCCATTATTTTCGTT 3960  
 3901 -----+-----+-----+-----+-----+-----+-----+  
 GAGCAACTAAAAAGTAGAGAATATTAGAGCGAAAACCAAAATTCTTCAAGATATTACC 4020  
 3961 -----+-----+-----+-----+-----+-----+-----+  
 TTTATTGATAATTATAGATGTTAATAAGCATATCTGAATGAAAGTCAGCAAAATATGT 4080  
 4021 -----+-----+-----+-----+-----+-----+-----+  
 GCGAAAACACCTGAAAAAAATCAAAATTCCTGCAGAAAATTGAGAAAATGCATTAAAATACA 4140  
 4081 -----+-----+-----+-----+-----+-----+-----+  
 TTTTGCACTTTCTACATCACATGAATGTAGAAAATTAAAAGGGAAATCAAATTTCTA 4200  
 4141 -----+-----+-----+-----+-----+-----+-----+  
 GAGGATATAATTGAATGAAACATTGCGAAATTAAATGTGCGAACGTCAAAAAGAGGA 4260  
 4201 -----+-----+-----+-----+-----+-----+-----+  
 |  
 AATTTGGGTATCAAATCGATCCTAAAACCAACACATTTCAGCATCCGCCAATCTTCAT 4320  
 4261 -----+-----+-----+-----+-----+-----+-----+  
 S A N S S F  
 180  
 TCACCGGATGCTCTCTCTCGGATACAGTTCAAGTCGAATCGCTCATTAGCAAGCTT 4380  
 4321 -----+-----+-----+-----+-----+-----+-----+  
 T G C S S L G Y S S S R N R S F S K A S  
 190 200  
 CTGGACCAACTCAATACATATTCCATGAAGAGGATATGAACTTGTGATGCACCAACCA 4440  
 4380 -----+-----+-----+-----+-----+-----+-----+  
 G P T Q Y I F H E E D M N F V D A P T I  
 210 220  
 TAAGCCGTGTTTCGACGAGAAAACCATGTACAGAAACTTCTCGAGTCCTCGTGGAAATGT 4500  
 4441 -----+-----+-----+-----+-----+-----+-----+  
 S R V F D E K T M Y R N F S S P R G M C  
 230 240  
 GCCTCATCATAATAATGAACACTTGGAGCAGATGCCAACCGGAATGGTACCAAGGCCG 4560  
 4501 -----+-----+-----+-----+-----+-----+-----+  
 L I I N N E H F E Q M P T R N G T K A D  
 250 260  
 ACAAGGACAATCTTACCAATTGTTAGATGCATGGCTATACGGTTATTTGCAAGGACA 4620  
 4561 -----+-----+-----+-----+-----+-----+-----+  
 K D N L T N L F R C M G Y T V I C K D N  
 270 280  
 | Intron 4  
 ATCTGACGGGAAGGGTACGGCGAAATTATATTACCCAAACCGCGAAATTGCCATTTGCG 4680  
 4621 -----+-----+-----+-----+-----+-----+-----+  
 L T G R



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## FIG. 4F

### Repeat 3

	----->	
4681	CCGAAAATGTGGCGCCCGGTCTGACACGACAATTGTGTTAAATGCAAAATGTATAAT	4740
4741	TTTGCAAAAAACAAAATTTGAACCTTCCGCAGAAATGATTTACCTAGTTTCGAAATTTC	4800
4801	GTTTTTCCGGCTACATTATGTGTTTTCTTAGTTCTATAATATTGATGTAAAAA	4860
4861	ACCGTTGTAAATTTCAGACAATTTCAGCATACAAAACCTGATAGCACGAAATCAATT	4920
4921	TTCTGAATTTCAAAATTATCCAAAATGCACAATTAAAATTGTGAAAATTGGCAAAC	4980
4981	GGTGTTCATGAAATGTATTTAAAAACTTAAACCCACTCCGGAAAAGCAATAA	5040
5041	AAATCAAAACACGTACAATTCAAATTCAAAGTTATTCCATCGATTGTTATTTTG	5100
5101	CAAAATTGAAAAAATCATGAAGGATTAGAAAAGTTTATAACATTTCTAGATT	5160
5161	TCAAAATTTTTAACAAATCGAGAAAAGAGAATGAAAATCGATTAAATATCC	5220

### Repeat 3

	-----^-----	
5221	ACAGCTCGAGAGTTGAAATTACAGTACTCCTAAAGCGCACACCCATTGCATTGG	5280
5281	ACCAAAAATTGCGTGTGAGACCAGGTACCGTAGTTTGTGCAAAATTGCACCAT	5340
5341	TGGACAATAACCTCTTAATCACCAAAAGTAAATTGAAATCTCGAAAAGCCAAA	5400
5401	ATTCAAAAAAAAGTCGAATTGATTTTTGGTTTTGGTCCCACCAAAACCAAA	5460
5461	AAATCAATTCTGCAAAATACCAAAAGAACCGAAAAATTCCCAGCCTGTCCT	5520
5521	AATGTAAACTGATATTAATTCCAGGAATGCTCTGACAATTGAGACTTGCCAAAC	5580
	G M L L T I R D F A K H 290	

5581	ACGAATCACGGAGATTCTGCGATACTCGTGTATCACACGGAGAAGAGAATGTGA	5640
	E S H G D S A I L V I L S H G E E N V I 310	

5641	TTATTGGAGTTGATGATACCGATTAGTACACACGGAGATATGATCTCTAACGCAG	5700
	I G V D D I P I S T H E I Y D L L N A A 330	



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## FIG. 4G

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A (n2433)  
| | Intron 5  
CAAATGCTCCCCGTCTGGCGAATAAGCCGAAATCGTTTGTGCAGGCTTGTCAAGGGCG  
5701 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 5760  
N A P R L A N K P K I V F V Q A C R G E  
350 360  
|  
GTTCGTTTTTATTTAATTTAATATAAATATTTAAATAATTTCATTTCAGAACGTC  
5761 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 5820  
R R  
|  
GTGACAATGGATTCCCAGTCTGGATTCTGTCGACGGAGTTCTGCATTCTTCGTCTG  
5821 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 5880  
D N G F P V L D S V D G V P A F L R R G  
370 380  
| T (n1165)  
GATGGGACAATCGAGACGGGCCATTGTTCAATTTCTTGATGTGTGCAGGCCGCAAGTC  
5881 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 5940  
W D N R D G P L F N F L G C V R P Q V Q  
390 400  
| Intron 6  
AGGTTGCAATTTAATTCTTGAATGAGAATATTCTTCAAAAATCTAAAATAGATT  
5941 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6000  
ATTCCAGAAAGTCCCAGTCGAAAAATTGCGATATAATTACGAAATTGTGATAAAATGAC  
6001 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6060  
Repeat 4  
----->  
AAACCAATCAGCATCGTCGATCTCGCCACTTCATCGGATTGGTTGAAAGTGGCGGA  
6061 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6120  
----->  
GTGAATTGCTGATTGGTCGCAGTTTCAGTTAGAGGAAATTAAAAATCGCCTTTCGA  
6121 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6180  
AAATTAAAAATTGATTTTCATTTTCGAAAAATTCCGATTATTATATTCTTT  
6181 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6240  
A (n717)  
|  
GGAGCGAAAGCCCCGTCTGAAACATTAAATGATAATTAATAATTGGCAGCAA  
6241 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6300  
Q  
| T (n1949)  
|  
GTGTGGAGAAAGAAGCCGAGCCAAGCTGACATTCTGATTGATACGCAACGACAGCTCAA  
6301 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 6360  
V W R K K P S Q A D I L I R Y A T T A Q  
410 420

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# FIG. 4H

A (n1286)

TATGTTCGTGGAGAACAGTGCTCGTGGATCATGGTCATTCAAGCCGTCTGTGAAGTG  
 6361 -----+-----+-----+-----+-----+-----+-----+ 6420  
 Y V S W R N S A R G S W F I Q A V C E V  
 430 440

T (n1129, n1164)

TTCTCGACACACGAAAGGATATGGATGTTGAGCTGCTGACTGAAGTCATAAGAAG  
 6421 -----+-----+-----+-----+-----+-----+ 6480  
 F S T H A K D M D V V E L L T E V N K K  
 450 460

T (n2430)

A (n2426)

| | Intron 7

GTCGCTTGTGGATTCAGACATCACAGGGATCGAATATTTGAAACAGATGCCAGAGGTA  
 6481 -----+-----+-----+-----+-----+-----+ 6540  
 V A C G F Q T S Q G S N I L K Q M P E  
 470 480

Repeat 5

CTTGAAACAAACAATGCATGTCTAACCTTAAGGACACAGAAAAATAGGCAGAGGCTCCT  
 6541 -----+-----+-----+-----+-----+-----+ 6600

----->

TTTGCAAGCCTGCCGCGTCAACCTAGAATTTAGTTTAGCTAAAATGATTGATT  
 6601 -----+-----+-----+-----+-----+-----+ 6660  
 GAATATTTATGCTAATTTTTGCGTTAAATTTGAAATAGTCACTATTATCGGGTT  
 6661 -----+-----+-----+-----+-----+-----+ 6720  
 CCAGTAAAAATGTTATTAGCCATTGGATTTACTGAAAACGAAAATTGTAGTTTC  
 6721 -----+-----+-----+-----+-----+-----+ 6780  
 AACGAAATTATCGATTTAAATGAAAAAAAAATAGCGAAAATTACATCAACCATAA  
 6781 -----+-----+-----+-----+-----+-----+ 6840  
 GCATTTAAGCCAAAATTGTTAACTCATTAAAAATTAAATTCAAAGTTGCCACGAGTATT  
 6841 -----+-----+-----+-----+-----+-----+ 6900

Repeat 5

<-----

ACACGGTTGGCGCGCGCAAGTTGCAAAACGACGCTCCGCCTCTTTCTGTGCCGCTT  
 6901 -----+-----+-----+-----+-----+-----+ 6960

T (n1163)

-----  
 GAAAACAAGGGATCGGTTAGATTTCCCCAAATTAATTAAATTTCAGATGACATC  
 6961 -----+-----+-----+-----+-----+-----+ 7020  
 M T S

CCGCCTGCTCAAAAGTTCTACTTTGCCGGAAGCAGAACTCTGCCGTCTAAATTC

7021 -----+-----+-----+-----+-----+-----+ 7080  
 R L L K K F Y F W P E A R N S A V \*  
 490 500



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## FIG. 4I

ACTCGTGATTCATGCCAATTGATAATTGTCTGTATCTTCTCCCCAGTTCTTTGC  
7081 -----+-----+-----+-----+-----+-----+ 7140  
CCAATTAGTTAAAACCATGTGTATATTGTTATCCTATACTCATTCACTTATCATTCT  
7141 -----+-----+-----+-----+-----+-----+ 7200  
ATCATTCTCTTCCCATTTCACACATTCCATTCTACGATAATCTAAAATTATGAC  
7201 -----+-----+-----+-----+-----+-----+ 7260  
GTTTGTGTCTCGAACGCATAATAATTAACTCGTTTGAAATTGATTAGTTGTTGT  
7261 -----+-----+-----+-----+-----+-----+ 7320  
GCCCAGTAGTATATGTATGTACTATGCTTCTATCAACAAAATAGTTCATAGATCATCACC  
7321 -----+-----+-----+-----+-----+-----+ 7380  
CCAACCCCACCAACCTACCGTACCATATTCAATTGGCCGGGAATCAATTGATTAAATT  
7381 -----+-----+-----+-----+-----+-----+ 7440  
TTAACCTATTTTCGCCACAAAAATCTAATATTGAATTAACGAATAGCATTCCCATC  
7441 -----+-----+-----+-----+-----+-----+ 7500  
TCTCCCGTGCCGGAAATGCCCTCCGGCTTTAAAGTTCGAACATTGGCAATTATGTAT  
7501 -----+-----+-----+-----+-----+-----+ 7560  
AAATTGTAGGTCCCCCCCATCATTCCGCCATCATCTCAAATTGCATTCTTTTCG  
7561 -----+-----+-----+-----+-----+-----+ 7620  
CCGTGATATCCCGATTCTGGTCAGCAAAGATCT  
7621 -----+-----+-----+-----+-----+ 7653

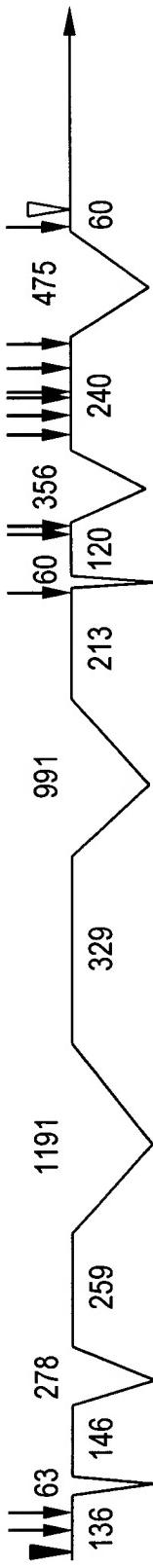
Title: CLONING, SEQUENCING AND CHARACTERIZATION  
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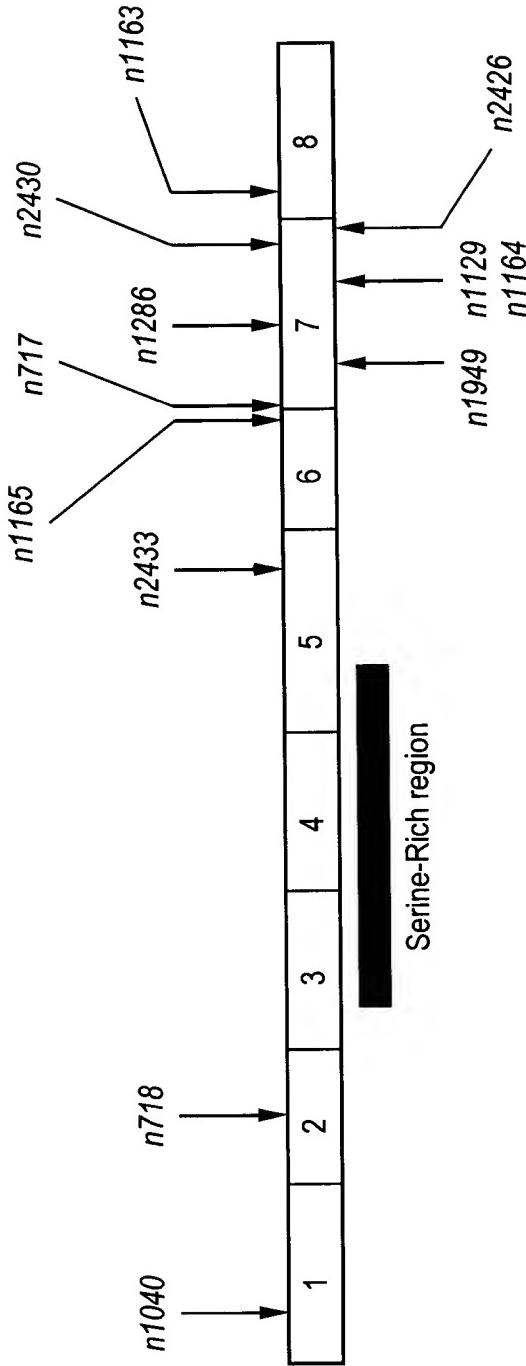
FIG. 5A



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## FIG. 5B

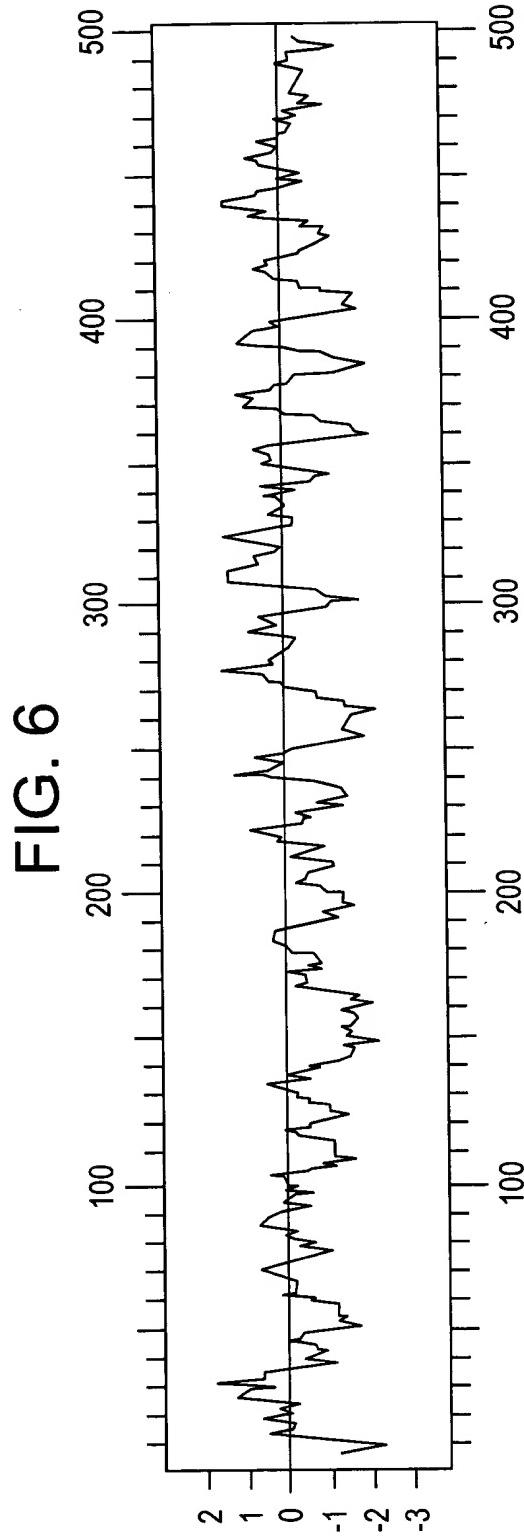
*ced-3* Mutations are Clustered





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## FIG. 7

## Lines

1 01 MMRQDRRLERNIMMFSSHLKVDEILEVLIAKQVLNSDNGDMINSCGTV 50  
2 .....W.....LE...K.QA.L.D.....V....R.E  
3 .....TVS.SLI..R.....M....

1 51 REKRREIVKAVQRPGDVAFDAFYDALRSTGHEGLAEVLEPLARSVDNAV 100  
2 ..DNEK.....R..E.....D..ND..D..M..S.P.....P.  
3

1 101 EFECPMSPASHRRSRALSPAGYTSPTRVHRDSVSSVSSFTS YQDIYSRA 149  
2 PM.....S.....P.A.....I.....T.V....  
3 S

1 150 RSRSR SRALHSSDRHNYSSPPVNAFPSQPSSANSSFTGCSSLGYSSSRN 198  
2 ..S..S..P.Q.....M\_AA\_TS.....A.....  
3 T.....P.T.....V.S..S.Q..A.....S.....T

1 199 RSFSKASGPTQYIFHEEDMFVDAPTISRVFDEKTMYRNFSSPRGMCLI 247  
2 .....T.AQS.....Y.....H.....L...  
3 .....Y.....AHS.....Y.....H.....T..L...

1 248 INNEHFEQMPTRNGTKADKDNLTNLFRCMGYTICKDNLTGRGMLLTIRD 297  
2 .....I.....E..S...S  
3 .....P..IS.....I.H.....M....

1 298 FAKHESHGDSAILVILSHGEENVIIIGVDDIPISTHEIYDILLNAANAPRLA 347  
2 ..GRNDM.....VSVNV.....  
3 ....N.T.....VSVNV...X.....

1 348 NPKKIVFVQACRGERRDNGFPVLDSDGVPAFLRRGWDNRDGPLNFLGC 397  
2 .....L.....SLI.....  
3 .....L.....V.....LI.....KG....

1 398 VRPQVQQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFIQAVCEVFST 447  
2 .....M..A.....L  
3 .....A.....A.....L

1 448 HAKDMVVELLTEVNKKVACGFQTSQGSNILKQMPEMTSRLKKFYFWPE 497  
2 .....L.....  
3 .....A.....L.....

1 498 ARN SAV 503  
2 DRG.....  
3 .....D..RS...

Line 1 C. elegans

Line 2 C. briggsae

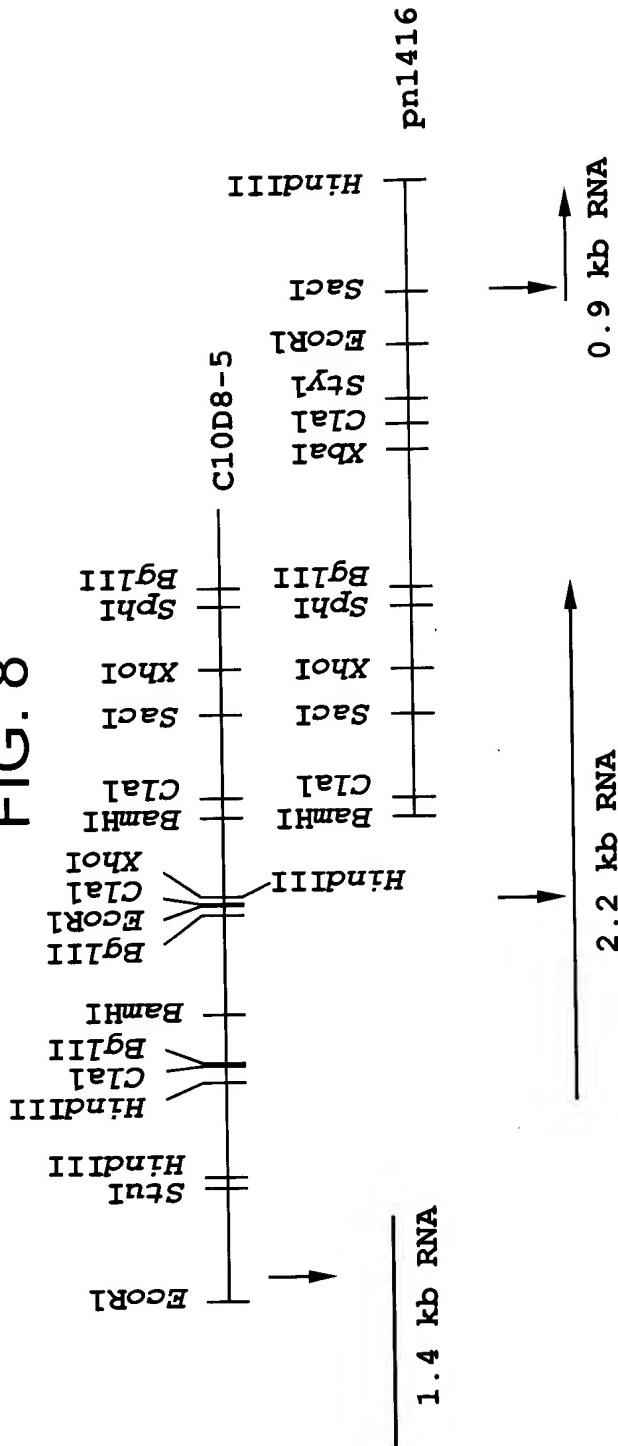
Line 3 C. vulgaris

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FIG. 8

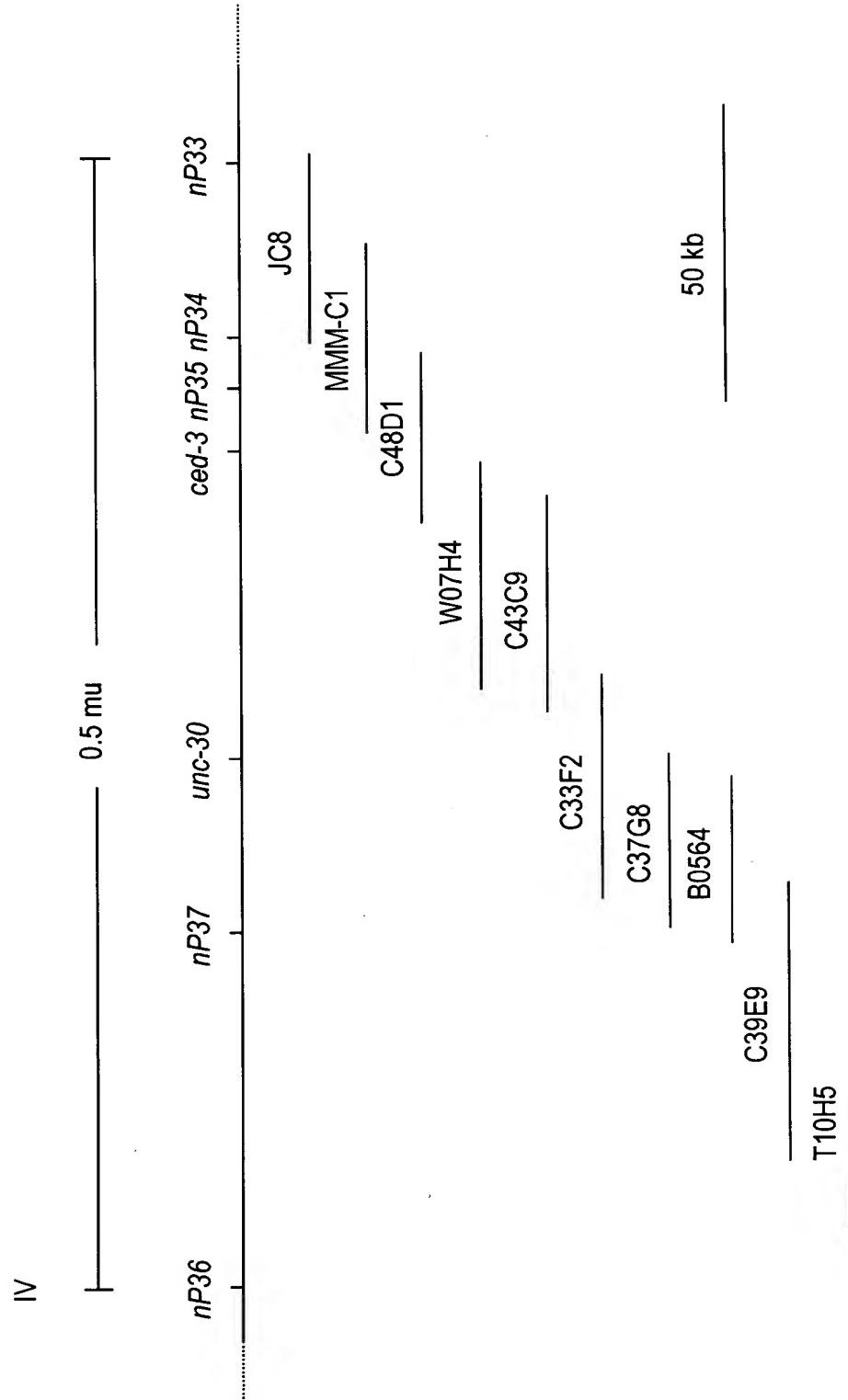




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## FIG. 9





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## FIG. 10

Summary of the experiments to localize *ced-3* gene within C40D1

